

Input file F1h14273new; Output File F1h14273tra  
Sequence length 1743

G	D	A	P	L	R	S	L	E	Q	A	N	R	T	R	F	P	F	S	29	
GCG	GAC	GCG	CCC	TTG	CGC	AGC	CTG	GAG	CAA	GCC	AAC	CGC	ACC	CGC	CCC	TTT	CCC	TTC	TCC	87
D	V	K	G	D	H	R	L	V	L	A	A	V	E	T	T	V	L	V	L	49
GAC	GTC	AAG	GCG	GAC	CAC	CGG	CTG	GTG	CTG	GCG	GCG	GTG	GAG	ACA	ACC	GTG	CTG	GTG	CTC	147
I	F	A	V	S	L	G	N	V	C	A	L	V	L	V	A	R	R	R	69	
ATC	TTT	GCA	GTC	TCG	CTG	GGC	AAC	GTG	TGC	GCC	CTG	GTG	CTG	GTG	GCG	GCG	CGA	CGA	207	
R	R	G	A	T	A	C	L	V	L	N	L	F	C	A	D	L	L	F	I	89
CGC	CGC	GCG	GCG	ACT	GCC	TGC	CTG	GTG	CTG	AAC	CTC	TTC	TGC	GCG	GAC	CTG	CTC	TTC	ATC	267
S	A	I	P	L	V	L	A	V	R	W	T	E	A	W	L	L	G	P	V	109
AGC	GCT	ATC	CCT	CTG	GTG	CTG	GCC	GTG	CGC	TGG	ACT	GAG	GCC	TGG	CTG	CTG	GCG	CCC	GTT	327
A	C	H	L	F	Y	V	M	T	L	S	G	S	V	T	I	L	T	L	129	
GCC	TGC	CAC	CTG	CTC	TTC	TAC	GTG	ATG	ACC	CTG	AGC	GGC	AGC	GTC	ACC	ATC	CTC	ACG	CTG	387
A	A	V	S	L	E	R	M	V	C	I	V	H	L	Q	R	G	V	R	G	149
GCG	GCG	GTC	AGC	CTG	GAG	CGC	ATG	GTG	TGC	ATC	GRG	CAC	CTG	CAG	CGC	GCG	GTG	CGG	GGT	447
P	G	R	R	A	R	A	V	L	A	L	I	W	G	Y	S	A	V	A	169	
CCT	CGG	CGG	CGG	CGG	CGG	CGG	GCA	GTC	CTG	GCG	CTG	ATC	TGG	GCC	TAT	TCG	GCG	GTC	GCC	507
A	L	P	L	C	V	F	F	R	V	V	P	Q	R	L	P	G	A	D	Q	189
GCT	CTG	CCT	CTC	TGC	GTC	TTC	TTT	CGA	GTC	CCG	CAA	CGG	CTC	CCC	GCC	GAC	GAC	CAG	567	

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TO FIG. 1B.

**FIG. 1A.**



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FROM FIG. 1A.

E	I	S	I	C	T	L	W	P	T	I	P	G	E	I	S	W	D	V	209	
GAA	ATT	TCG	ATT	TGC	ACA	CCTG	ATT	TGG	CCC	ACC	ATT	CCT	GGA	GAG	ATC	TCG	TGG	GAT	GTC	627
S	F	V	T	L	N	E	L	V	P	G	L	V	I	V	I	S	Y	S	K	229
TCT	TTT	GTT	ACT	TTG	AAC	TTC	TTC	GTG	CCA	GGA	CTG	GTC	ATT	GTG	ATC	AGT	TAC	TCC	AAA	687
I	L	Q	I	T	K	A	S	R	K	R	L	T	V	S	L	A	Y	S	E	249
ATT	TTA	CAG	ATC	ACA	AAG	GCA	TCA	AGG	AAG	AGG	CTC	ACC	GTA	AGC	CTG	GCC	TAC	TCG	GAG	747
S	H	Q	I	R	V	S	Q	Q	D	F	R	L	F	R	T	L	F	L	L	269
AGC	CAC	CAG	ATC	CGC	GTG	TCC	CAG	GAC	TTC	CGG	CTC	TTC	CGC	ACC	CTC	CTC	CTC	CTC	CTC	807
M	V	S	F	I	M	W	S	P	I	I	T	I	L	L	I	L	I	L	I	208
ATG	GTC	TCC	TTC	TTC	ATC	ATG	TGG	AGC	CCC	ATC	ATC	ACC	ATC	CTC	CTC	CTC	ATC	CTG	ATC	867
Q	N	F	K	Q	D	L	V	I	W	P	S	L	F	W	V	V	A	F	309	
CAG	AAC	TTC	AAG	CAA	GAC	CTG	GTC	ATC	TGG	CCG	TCC	CTC	TTC	TGG	GTG	GCC	TTC	927		

TO FIG. 1C.

**FIG. 1B.**



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FROM FIG. 1B.

T	F	A	N	S	A	L	N	P	I	L	Y	N	M	T	L	C	R	N	E	
ACA	TTT	GCT	AAT	TCA	GCC	CCC	ATC	CTC	TAC	AAC	ATG	ACA	CTG	TGC	AGG	AAT	GAG	987	329	
W	K	K	I	F	C	C	F	W	F	P	E	K	G	A	I	L	T	D	T	
TGG	AAG	AAG	AAA	ATT	TTT	TGC	TGC	TTC	TGG	TTC	CCA	GAA	AAG	GGA	GCC	ATT	TTA	GAC	ACA	1047
S	V	K	R	N	D	L	S	I	I	S	G	•	362							
TCT	GTC	AAA	AGA	AAT	GAC	TTG	TGC	ATT	ATT	TCT	GGC	TAA	1086							

TTTTCTTTATAGGCCGAGCTTCTCACACCTGGCGAGGCTGTGGCATGCTTTAAACAGAGTCATTTCAGTACCCCTCCA  
 TCAGTGCACCCCTGCTTTAAGAAAATGAACCTATGCAAATAGACATCCACAGCGTCGGTAATTAAAGGGGTGATCACCAA  
 GTTTCATATAATTTCCTTTATAAAAGGATTGTGTTGCCAGGTGCAGTGTTCATGCCCTGTAATCCCAGCAGTTGGG  
 AGGCTGAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAACCTGACCAACATGGTAGACCACCGCTCTACTA  
 AAAATAAAAAAAATTAGCTGGGAGTGGTGGTGGCACCTGTAATCCTAGCTACTGGGAGGCTGAACCAGGAGAAT  
 CTCTTGAACCTGGGAGGGCAGAGTTGCAAGTGAAGCOGAGATOGTGCCATTGCACTCCAACCAAGGGCAACAAGAGTGAAAC  
 TCCATCTTAAAAAAAGATTTGTTATGGGTTCCCTTTAAATGTGAACTTTTAGTGTGTTGTAATATG  
 ATCAAATTAAATATTATTTATGACTGTTCAAGCAAAAAAAAAAGGGCGG

RTA01/2057957v1

**FIG. 1C.**



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Sequence	Description	score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin)	119.9	4.7e-37	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value	-
7tm_1	1/1	57	321	1	259	[ ]	119.9	4.7e-37

Alignments of top-scoring domains:

7tm\_1: domain 1 of 1, from 57 to 321: score 119.9, E = 4.7e-37  
 \*->GN1LVi1vi1rtkk1rtptnifi1NLAVADLLf11t1ppw1yy1vg

GN+ ++++++r ++r +t +++1NL ADLLf + p++ ++ -+

F1h14273, 57 GNVCALVLVAR-RRRRGATACLVNLFCADLLFISAIPVLAVR-WT 101

gaadWpfGsa1Ck1vtaldvvnmyaS111Lta1S1DRY1A1vhP1ryrrr  
 e W++G++ C+1+ +++++++ + i1+L+a S++R + Iv 1+ +r

F1h14373, 102 --EAWLLGPVACHLLFYYMTLSGSVTILTLAAVSLERMVVCIV-HLQRGVR 148

rtsprrAkvv11vwv1a111s1Pp11fswvktveegngt1nvnevC1;  
 +r +v+++1+W +++++1P +f+ v+ ++ ++ ++ +C++

F1h14273, 149 GPGRRARAVLLALIWGYSAVAALPLCVFFRVVPQRLPG--ADQEISICTL 196

dfpccstasvstw1rsyv11st1wgF11P11vi1vcYtr11rt1r....  
 +p++++ +t+st +++ ++ F1+P 1vi++ Y+ I1 + + +++++

F1h14273, 197 IWPTIPG--xer-EISWRVSFTLNELVRGLVIVISYSKILQITKasrkr 240

..... kaakt11vvvvvFv1CW1Pyfi111dt1c  
 + + +++++ + + + + +t1++++v F++ W P i++11 +

F1h14273, 241 1cvslayseehqirvsqqdfRLFRTLFLLMVSFFIMWSPIIITILLILIQ 290

.1siimsstCe1erv1pta11vt1wLayvNsc1NPi1Y<-\*  
 +- + + p +++++ + +++++Na+1NPi+Y

F1h14273, 291 nFK-----QDLVIWPSLFVVVAPTAFANSALNPILY 321

**FIG. 2.**

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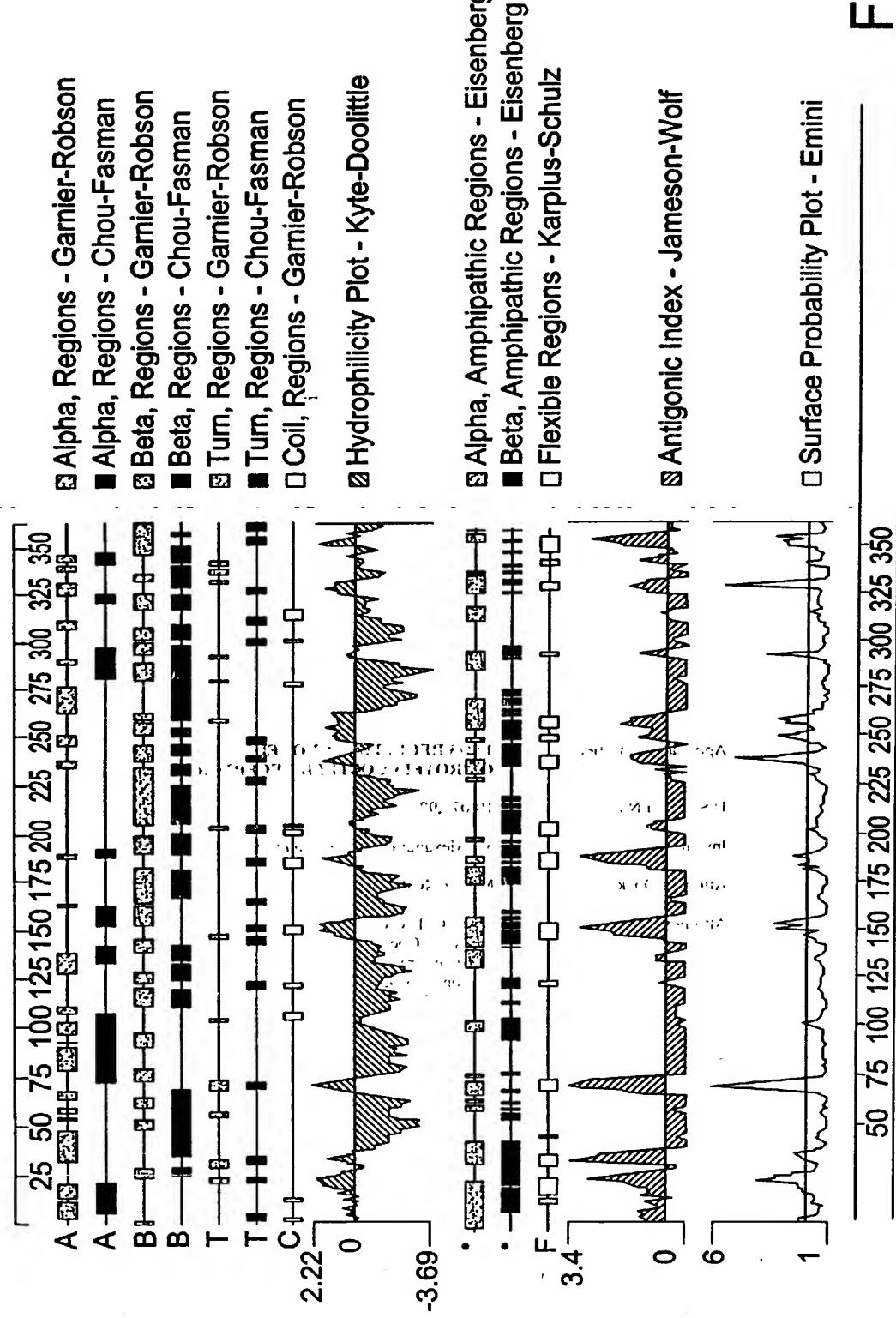


FIG. 3.

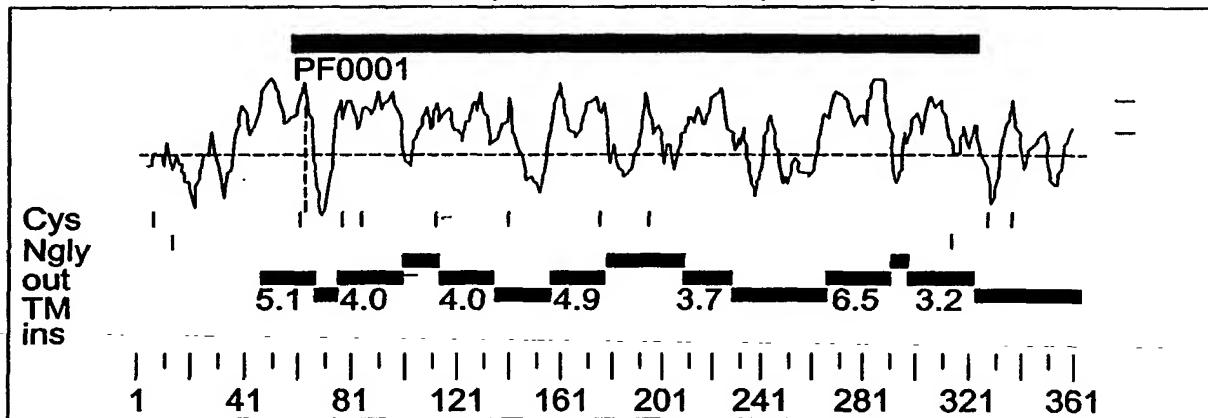


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### Analysis of Flh14273, (362 aa)



>Flh14273, 1086 bases, 1825 checksum.  
MSPECARAQDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVLEFAVSLGNVC  
ALVLVARRRRRGATAQLVLNLFCADLLFYSAIPLVLA VRVTEAVLLGPVACHLLFYVMTL  
SGSVTILTAAVSLERMVCIVHLQRCVRGPGRARAVLLALIWGYSAVAALPLCVFFRVV  
PQRPGADQEISICTLIWPTIPGEISWDVSFVTLNFLYPGLVIVISYSKILQITKASRKR  
LTVSLAYSESHQIRVSQQIDRLFRTLFLLMVSFFIMWSPIITILLILIQNFKQDLVIWP  
SLFFWVAFTFANSALNPILYNMTLCRNEWKKIFCCPWFPEKGAILTDTSVKRNDLSIIS  
G+

**FIG. 4.**

Prosite Pattern Matches for F1h14273

>PS00001/PDC00001/ASN\_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTR 24

Query: 322 NMNL 325

>PS0004/PDC00004/CAMP\_PHOSPHO\_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 239 KRLT 242

>PS00005/PDC00005/PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 237 SRK 239

Query: 350 SVK 352

>PS00006/PDC00006/GK2\_PHOSPHO\_SITE Casien kinase II phosphorylation site.

Query: 256 SQQQ 259

>PS00008/PDC00008/MYRISTYL N-myristoylation site.

Query: 57 GNVCAL 62

Query: 72 GATACL 77

Query: 343 GAILTD 348

>PS00009/PDC00009/AMIDATION Amidation site.

Query: 150 PCRR 153

>PS00029/PDC00029/LEUCINE\_ZIPPER Leucine zipper pattern.

Query: 106 LGPVACHLLFYVMTLSGSVTIL 127



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FIG. 5.



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### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
75	98	ins->out	4.0
113	134	out->ins	4.0
156	177	ins->out	4.9
209	227	out->ins	3.7
266	289	ins->out	6.5
297	321	out->ins	3.2

>F1h14273,  
MSPECARAAGDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVLIPAVSLLGNVC  
ALVLVARRRRRGATACLVNLFCADLLFISAWPLVLAVRTEAWLLGPVACHLLFYVMTL  
SGSVTILTLAAVSLERMVCIVHLQRGVRGPGRARAVLLALIWGYSAVAALPLCVFFRVV  
PQLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKR  
LTSLAYSESHQIRVSQQDFRLFRRTLFLMVSFFIMWSPIIITILLILIQNFKQDLVIWPS  
SLFFWVVAFTFANSALNPILYNMTLCRNEWKKIFCCFWFPEKGAILTDTSVKRNDLSIIS  
G

### Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
14	37	ins->out	4.0
52	73	out->ins	4.0
95	116	ins->out	4.9
148	166	out->ins	3.7
205	228	ins->out	6.5
236	260	out->ins	3.2

>F1h14273, \_mature  
LVLVARRRRRGATACLVNLFCADLLFISAIPLVLAVRTEAWLLGPVACHLLPYVMTLS  
GSVTILTLAAVSLERMVCIVHLQRGVRGPGRARAVLLALIWGYSAVAALPLCVFFRVVP  
QRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVISYSKILQITKASRKRL  
TVSLAYSESHQIRVSQQDFRLFRRTLFLMVSFFIMWSPIIITILLILIQNFKQDLVIWPS  
LFFWVVAFTFANSALNPILYNMTLCRNEWKKIPCCFWFPEKGAILTDTSVKRNDLSIISG

**FIG. 6.**



Input file 14273mj Output File 14273mtra  
Sequence length 1560  
TTGCCAAGCTCAGCGTAAGCCTTTCAACTGCAATCTCACAGGGAGTCGATGACCCCTCTTGACAGGCCACGAAGCCGGCAGGCTC

	M	S	P	E	C	A	Q	T	T	G	10	
P	G	P	S	H	T	L	D	Q	V	N	R	30
CCT	GCT	CCC	TGG	CAC	ACC	CTG	GAC	CAA	GTC	AAT	CGC	30
V	K	G	D	H	R	L	V	E	S	V	E	90
GTC	AAG	GGC	GAC	CAC	CGG	TGG	GTC	TGG	AGC	GTC	GAG	150
F	V	V	S	L	N	L	V	A	L	V	L	150
TTT	GTC	GTC	TCA	CTG	CTG	GGC	AAC	TGG	TGT	GCT	CTG	150
R	G	A	S	A	S	L	V	L	N	L	F	70
CGT	GGG	GCG	TCA	GCC	AGC	CTG	GTC	CTC	AAC	CTC	TTC	210
A	I	P	L	V	L	V	R	W	T	E	A	90
GCC	ATC	CCT	CTA	GTC	CTC	GTC	GTC	TGG	ACT	GAG	GCC	270
C	H	L	L	F	Y	Y	M	T	M	S	G	330
TGC	CAC	CTG	CTC	TTC	TAC	GTC	ATG	ACA	ATG	AGC	AGC	390
A	V	S	L	E	R	M	V	C	I	V	R	130
GCG	GTC	AGC	CTG	GAG	CGC	ATG	GTC	TGG	TGG	CGC	CGC	150
G	R	R	T	Q	A	A	L	L	A	F	I	450
GGG	CGG	CGG	ACT	CAG	GCG	GCA	CTG	CTG	GCT	TTC	TAC	510

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TO FIG. 7B

FIG. 7A.

FROM FIG. 7A.



L	P	L	Y	I	L	F	R	V	P	Q	R	L	P	G	G	D	Q	E		
C	CCC	CTC	TAC	ATC	TTC	CGC	GTC	GTC	CCG	CAG	GGC	CTT	CCC	GGC	GAA	CAG	GAA	1927		
I	P	I	C	T	L	D	W	P	N	R	I	G	E	I	S	W	D	F		
ATT	CCG	ATT	TGC	ACA	TTG	GAT	TGG	CCC	AAC	CGC	ATA	GGA	GAA	ATC	TCA	TGG	GAT	GTG	210 630	
F	E	T	L	N	F	L	V	P	G	L	V	I	V	I	S	Y	S	K		
TTT	GAG	ACT	TTG	AAC	TTC	CTG	GTG	CCG	GGA	CTG	GTC	ATT	GTG	ATC	AGT	TAC	TCC	AAA	ATT	230 690
L	Q	I	T	K	A	S	R	K	R	L	T	L	S	L	A	Y	S	E		
TTA	CAG	ATC	ACG	AAA	GCA	TGG	CGG	AAG	AGG	CTT	ACG	CTG	AGC	TTG	GCA	TAC	TCT	GAG	AGC	250 750
H	Q	I	R	V	S	Q	Q	D	Y	R	L	F	R	T	L	F	L	M		
CAC	CAG	ATC	CGA	GTC	TCC	CAA	CAA	SAC	TAC	CGA	CTC	TTC	CGC	CGC	AGC	CTC	TTC	CTG	ATC	270 810
V	S	F	F	I	M	W	S	P	I	I	T	I	L	L	I	L	I	Q	290	
GTT	TCC	TTC	TTC	ATC	ATG	TGG	AGT	GGC	ATC	ATC	ACC	ATC	ATC	CTC	CTC	ATC	ATC	CAA	870	
N	F	R	Q	D	V	I	V	P	S	L	F	F	W	V	A	F	T	T	310	
AAC	TTC	CGG	CAG	GAC	CTG	GTC	GTC	ATC	TGG	CCA	TCC	CTT	TTC	TTC	TGG	GTG	GCC	TTC	AUG	930
F	A	N	S	A	L	N	P	I	L	Y	N	M	S	L	F	R	N	E		
TTT	GCC	AAC	TCT	GCC	CTA	AAC	CCC	ATA	CTG	TAC	AAC	ATG	TGG	CTG	TTC	AGG	AAC	GAA	TGG	330 990
R	K	I	F	C	C	F	F	F	P	E	K	G	A	I	F	T	D	T	S	350
AGG	AAG	ATT	TTT	TGC	TGC	TTC	TTT	TTT	CCA	GAG	AAG	GGA	GGC	ATT	TTT	ACA	GAT	ACG	TCT	1050
V	R	R	N	D	L	S	V	V	I	S	S	*							362 1086	
GTC	AGG	CGA	AAT	GAC	TTG	TCT	GTT	ATT	TCC	AGC	TA									

CTAGCCTCTGGTGCAGGTGAACCAAGGGTGTGCATGTAAGGAAAGCCCACCAAGTGCGCCCTGC  
TTAAAAATAACCGGACTTCCAACAGCAGGCATCTACGGAGCCATTGTTGTAATATGATCTAGTTAATAAATT  
TTTATTATAACGTGTTCCATACAAAAAAAGAAAAAA

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FIG. 7B.



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Query: 14273m,

Scores for sequence family classification (score includes all domains):

Sequence	Description	Score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin)	118.8	1e-35	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
7tm_1	1/1	57	321 ..	1	259 [ ]	118.8	1e-36

### Alignments of top-scoring domains:

7tm\_1: domain 1 of 1, from 57 to 321; score 118.8, E = 1e-36  
\*->GN1LVi1v11rtkk1rtptnifi1NLAvADLLf11t1ppwa1yy1vg

14273m. 57 GNV CAL VL VAR-RRRRRGASASL VL NL FC AD LL FT SA I PL VL VVR-WT 101

gaadWpfGaa1Ck1vtaldvvnmyaS;111Lta1S;DRY1A1vhP1ryrrr  
e W++G+++C+1+ +++++++ + ;1+L+a S++R + Iv lr +

14273m, 102 --EAWLLGPVVCHLLPYVMTMSGVTILTLAAVSLERMVCIV-RLRRGLS 148

rtsprRA. kvv i11vWv1a111s1Pp11fswvktveagngt1nvnvttvC1  
rr++++++W ++1++1P +++++ v + ++9 + +tC+

14273m, 149 GP-GRRTqAALLAFIWGYSALAAPPLYILFRVVPQRLLPGGD--QEITPC 195

idfppeestasvstw1rsyv11st1vgF21P11v1voYtr11rt1r....  
+dtp++ +

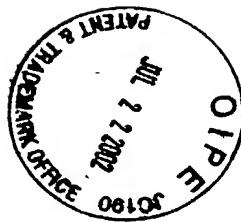
14273m. 196 | DWPNRIG-----FISWDPVEFTI NEI VPGI VIVISYSKII QITKasrk 239

14273m, 240 ritlslayseshqirvsqddyRLFRTLFLLMVSFFPMWSPIIIITILLILI 289

c. 1aiimestCelerVipta11vt1wLoyvNsc1NP; i1Y<-\*

14273m 290 QnER-----QDI VIVPSI FEWVVAETEANSANPTELY 321

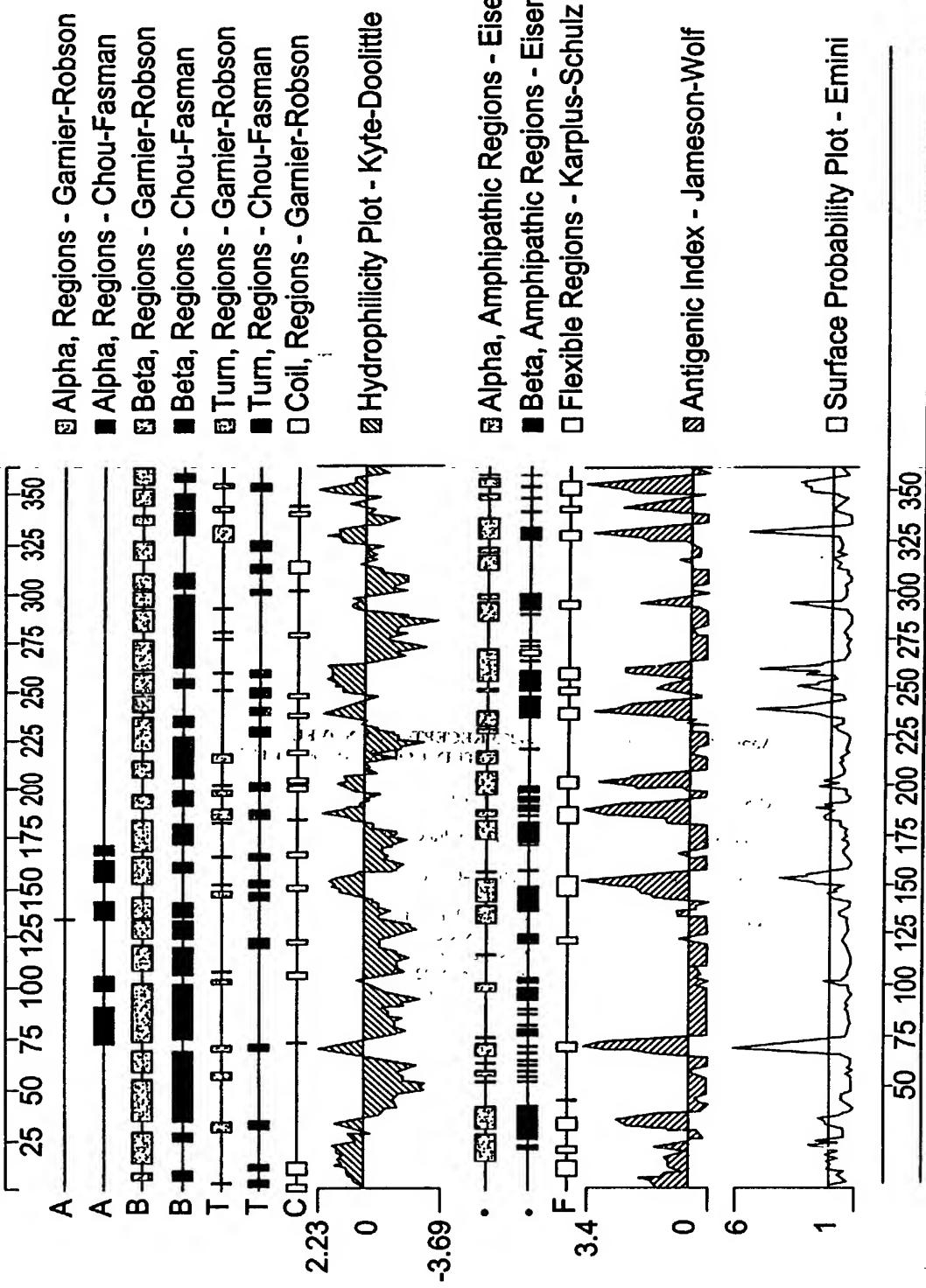
### FIG. 8.



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**FIG.**

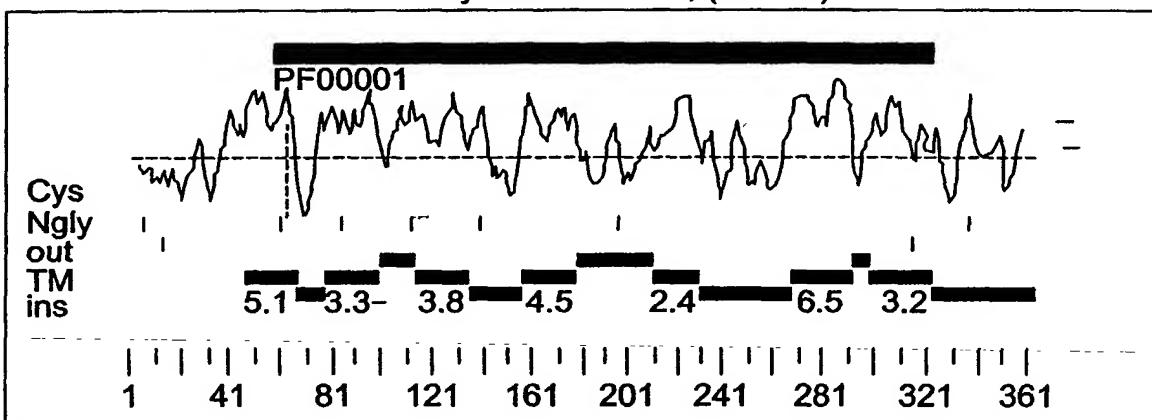


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Analysis of 14273m, (362 aa)



>14273m, 1086 bases, 6943 checksum.  
MSPECAQTTGPCPSHTLDQVNRTHFPPFSDVKGDHRLVLSVETTVLGLIFVVSLGNVC  
ALVLVARRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFVVM  
SGSVTILTAAVSLERMVCIVRLRRGLSGPGRTQAALLAFIWGYSALAALPLYILFRVV  
PQRLPGGDQEIPICTLDPNRIGEISWDVFFETLNFLVPGLVIVISYSKILQITKASRKR  
LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSSFIWSPIIIITILLILIQNFRQDLVIWP  
SLFWVVAFTFANSALNPILYNMSLFRNEWRKIFCCFPPEKGAIFTDTSVRRNDLSVIS  
S\*

FIG. 10.



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Prosite Pattern Matches for 14273m,

>PS00001/PDDC00001; ASN\_GLYCOSYLATION N-glycosylation site.

Query: 21      NRTH    24  
Query: 322     NRTH    325

>PS00002/PDDC00002/GLYCOSAMINOGLYCAN Glycosaminoglycan attachment site.

RU      Additional rules:

RU      There must be at least two acidic amino acids (Glu or Asp) from -2 to -4 relative to the serine.

Query: 148     SGPG    151

>PS00004/PDDC00004/CAMP\_PHOSPHO\_SITE cAMP- and cGMP-dependent protein kinase phosphorylation

Query: 239     KRLT    242

>PS00005/PDDC00005/PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 237     SRK     239  
Query: 350     SVR     352

>PS00006/PDDC00006/CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 40      SVVE    43  
Query: 256     SQQD    259

>PS00008/PDDC00008/MYRISTYL N-myristoylation site.

Query: 57      GNVCAL 62  
Query: 72      GASASL 77  
Query: 343     GAIFTD 348

>PS00009/PDDC00009/AMIDATION Amidation site.

Query: 150     PGRR    153

FIG. 11.



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### Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
77	98	ins->out	3.3
113	134	out->ins	3.8
156	177	ins->out	4.5
209	227	out->ins	2.4
266	289	ins->out	6.5
297	321	out->ins	3.2

>14273m,

MSPECAQTTGPGPSHTLDQVNRTHFPPFSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC  
ALVLVARRRRRGASASLVLNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMTM  
SGSVTILTAAVSLERMVCIVRLRRLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV  
PQLPQGDQEIPICTLDWPNRIGEISWDVFFETLNFLVPGLVIVISYSKILQITKASRKR  
LTLSLAYSESHQIRVSQQDYRLFRTLFLLMVSFFIMWSPIIIITILLILIQNFRQDLVIWP  
SLFFFVVVAFTFANSALNPILYMMMSLFRNEWRKIFCCFFFPEKGAIIFTDTSVRRNDLSVIS  
S

### Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
16	37	ins->out	3.3
52	73	out->ins	3.8
95	116	ins->out	4.5
148	166	out->ins	2.4
205	228	ins->out	6.5
236	260	out->ins	3.2

>14273m, \_mature

LVLVARRRRRGASASLVLNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCHLLFYVMGMS  
GSVTILTAAVSLERMVCIVRLRRLSGPGRRTQAIIIAFIWGYSALAALPLYILFRVVP  
QRLPQGDQEIPICTLDWPNRIGEISWCVFFETLNFLVPGLVIVISYSKILQITKASRKL  
TLSLAYSESKQIRVSQQDYRLFRTLFLLMVSFFTMWSPIIIITILLILIQNFRQDLVIWPS  
LFFFVVVAFTFANSALNPILYMMMSLFRNEWRKIFCCFFFPEKGAIIFTDTSVRRNDLSVISS

**FIG. 12.**